In the Claims

Please amend claims 1, 4, 5, 8, 13, 14, and 15 as shown below.

1. (Currently amended) A first hybridization assay probe for use in determining the presence of HPV Type 16 nucleic acid in a sample, wherein the base sequence of said first probe is up to 100 bases in length and consists of a first target binding region having no more than ~~about~~ a 10% base difference with a base sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 and SEQ ID NO:8 and, optionally, additional nucleotides that are non-complementary to nucleic acid derived from HPV Type 16 adjacent the complement of said first target binding region, wherein said first probe forms a detectable probe:target duplex with a first target nucleic acid sequence derived from HPV Type 16 under selective stringency hybridization conditions, and wherein said first probe does not form a detectable probe:non-target duplex with nucleic acid derived from HPV Type 18 under said conditions.

2. (Previously amended) A nucleic acid hybrid formed between said first probe and said first target nucleic acid sequence of claim 1.

3. (Canceled)

4. (Currently amended) A kit comprising:

said first probe of claim 1; and

a set of amplification oligonucleotides for use in amplifying HPV Type 16 nucleic acid in a sample, said set including:

a first amplification oligonucleotide, wherein the base sequence of said first amplification oligonucleotide consists of a first base region having no more than ~~about~~ a 20% base difference with a base sequence selected from the group consisting

of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4 and, optionally, a second base region that is recognized by an RNA polymerase; and

a second amplification oligonucleotide, wherein the base sequence of said second amplification oligonucleotide consists of a first base region having no more than ~~about~~ a 20% base difference with a base sequence selected from the group consisting of SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87 and SEQ ID NO:88, and, optionally, a second base region that is recognized by an RNA polymerase.

5. (Currently amended) A kit comprising:

said first probe of claim 1; and

a second hybridization assay probe for use in determining the presence of HPV Type 18 nucleic acid in a sample, wherein the base sequence of said second probe is up to 100 bases in length and consists of a second target binding region having no more than ~~about~~ a 10% base difference with a base sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47 and SEQ ID NO:48 and, optionally, additional nucleotides that are non-complementary to nucleic acid derived from HPV Type 18 adjacent the complement of said second target binding region, wherein said second probe forms a detectable probe:target duplex with a second target nucleic acid sequence derived from HPV Type 18 under said conditions, and wherein said second probe does not form a detectable probe:non-target duplex with nucleic acid derived from HPV Type 16 under said conditions.

6. (Canceled)

7. (Canceled)

8. (Currently amended) The kit of claim 5 further comprising a helper probe,

wherein the base sequence of said helper probe has no more than ~~about~~ a 10% base difference with a base sequence selected from the group consisting of SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123 and SEQ ID NO:124, wherein said helper probe binds to nucleic acid derived from HPV Type 18 under said conditions, thereby facilitating hybridization of said second probe to said second target nucleic acid sequence.

9. (Canceled)

10. (Canceled)

11. (Withdrawn - Original) A method for determining the presence of HPV Type 16 nucleic acid in a sample, said method comprising the steps of:

providing to a sample said first probe of claim 1 under said conditions; and

determining whether said probe:target duplex has formed as an indication of the presence of HPV Type 16 nucleic acid in said sample.

12. (Canceled)

13. (Withdrawn - Currently amended) The method of claim 11 further comprising providing to said sample a set of amplification oligonucleotides, said set including:

a first amplification oligonucleotide, wherein the base sequence of said first amplification oligonucleotide consists of a first base region having no more than ~~about~~ a 20% base difference with a base sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4 and, optionally, a second base region that is recognized by an RNA polymerase; and

a second amplification oligonucleotide, wherein the base sequence of said

second amplification oligonucleotide consists of a first base region having no more than ~~about~~ a 20% base difference with a base sequence selected from the group consisting of SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87 and SEQ ID NO:88 and, optionally, a second base region that is recognized by an RNA polymerase.

14. (Withdrawn - Currently amended) The method of claim 11 further comprising providing to said sample a second hybridization assay probe for use in determining the presence of HPV Type 18 nucleic acid in a sample, wherein the base sequence of said second probe is up to 100 bases in length and consists of a second target binding region having no more than ~~about~~ a 10% base difference with a base sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47 and SEQ ID NO:48 and, optionally, additional nucleotides that are non-complementary to nucleic acid derived from HPV Type 18 adjacent the complement of said second target binding region, wherein said second probe forms a detectable probe:target duplex with a second target nucleic acid derived from HPV Type 18 under said conditions, and wherein said second probe does not form a detectable probe:non-target duplex with nucleic acid derived from HPV Type 16 under said conditions.

15. (Withdrawn - Currently amended) The method of claim 14 further comprising providing to said sample a helper probe, wherein the base sequence of said helper probe has no more than ~~about~~ a 10% base difference with a base sequence selected from the group consisting of SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123 and SEQ ID NO:124, wherein said helper probe binds to nucleic acid derived from HPV Type 18 under said conditions, thereby facilitating hybridization of said second probe to said second target nucleic acid sequence.

Claims 16.-19. (Canceled)

20. (Previously presented) The probe of claim 1, wherein said first target binding region consists of a base sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 and SEQ ID NO:8.

21. (Previously presented) The probe of claim 1, wherein the base sequence of said first probe consists of a base sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 and SEQ ID NO:8.

22. (Previously presented) The probe of claim 1, wherein said first probe is labeled with a reporter group moiety.

23. (Previously presented) The kit of claim 4, wherein:

said first target binding region consists of a base sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 and SEQ ID NO:8;

said first base region of said first amplification oligonucleotide consists of a base sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4; and

said first base region of said second amplification oligonucleotide consists of a base sequence selected from the group consisting of SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87 and SEQ ID NO:88.

24. (Previously presented) The kit of claim 23, wherein the base sequence of said first probe consists of a base sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 and SEQ ID NO:8.

25. (Previously presented) The kit of claim 4, wherein at least one of said first and second amplification oligonucleotides further consists of said second base region.

26. (Previously presented) The kit of claim 5, wherein:

said first target binding region consists of a base sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 and SEQ ID NO:8; and

said second target binding region consists of a base sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47 and SEQ ID NO:48.

27. (Previously presented) The kit of claim 5, wherein:

the base sequence of said first probe consists of a base sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 and SEQ ID NO:8; and

the base sequence of said second probe consists of a base sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47 and SEQ ID NO:48.

28. (Previously presented) The kit of claim 5, wherein each of said first and second probes is labeled with a reporter group moiety.

29. (Previously presented) The kit of claim 8, wherein:

said first target binding region consists of a base sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 and SEQ ID NO:8;

said second target binding region consists of a base sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47 and SEQ ID NO:48; and

the base sequence of said helper probe consists of the base sequence selected from the group consisting of SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123 and SEQ ID NO:124.

30. (Previously presented) The kit of claim 29, wherein:

the base sequence of said first probe consists of a base sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 and SEQ ID NO:8; and

the base sequence of said second probe consists of a base sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47 and SEQ ID NO:48.